FIG. 1A

```
  1  agggagaggc agtgaccatg aaggctgtgc tgcttgccct gttgatggca
 51  ggcttggccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc
101  ccaggtgagc aacgaggact gcctgcaggt ggagaactgc acccagctgg
151  gggagcagtg ctggaccgcg cgcatccgcg cagttggcct cctgaccgtc
201  atcagcaaag gctgcagctt gaactgcgtg gatgactcac aggactacta
251  cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcca
301  gcggggccca tgccctgcag ccggctgccg ccatccttgc gctgctccct
351  gcactcggcc tgctgctctg gggacccggc cagctatagg ctctgggggg
401  ccccgctgca gcccacactg ggtgtggtgc cccaggcctt tgtgccactc
451  ctcacagaac ctggcccagt gggagcctgt cctggttcct gaggcacatc
501  ctaacgcaag tttgaccatg tatgtttgca ccccttttcc ccnaaccctg
551  accttcccat gggccttttc caggattccn accnggcaga tcagttttag
601  tganacanat ccgcntgcag atggcccctc caaccntttn tgttgntgtt
651  tccatggccc agcattttcc acccttaacc ctgtgttcag gcacttnttc
701  ccccaggaag ccttccctgc ccaccccatt tatgaattga gccaggtttg
751  gtccgtggtg tcccccgcac ccagcagggg acaggcaatc aggagggccc
801  agtaaaggct gagatgaagt ggactgagta gaactggagg acaagagttg
851  acgtgagttc ctgggagttt ccagagatgg ggcctggagg cctggaggaa
901  ggggccaggc ctcacatttg tggggntccc gaatggcagc ctgagcacag
951  cgtaggccct taataaacac ctgttggata agccaaaaaa aaaaaaaa
```

FIG. 1B

MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQV

ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS

QDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPAL

GLLLWGPGQL

FIG. 2

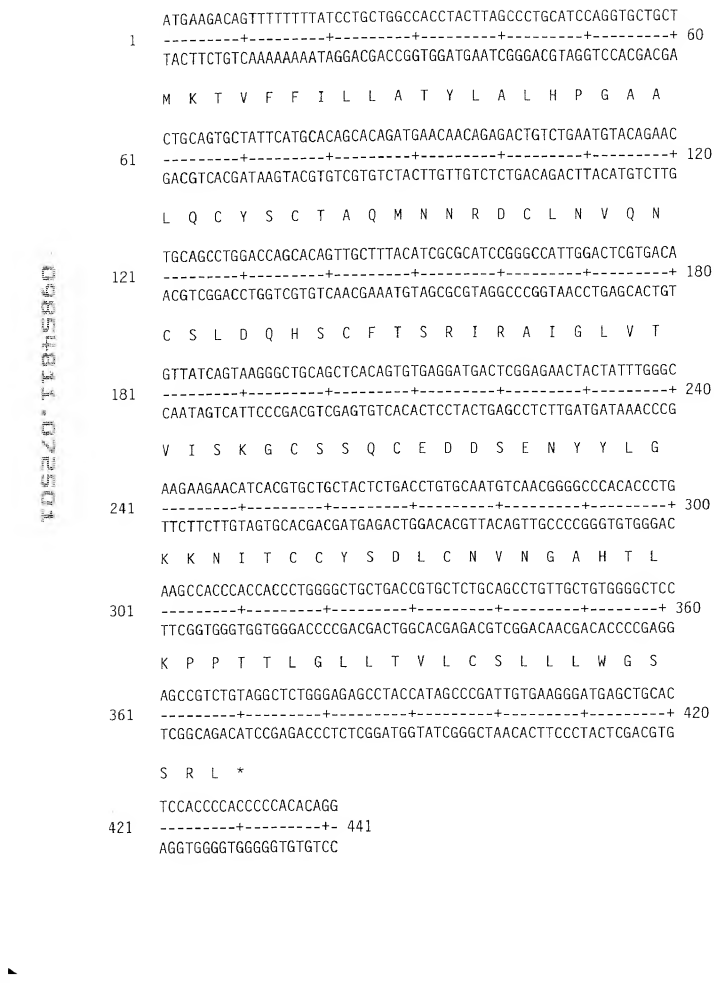

ATGAAGACAGTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT
TACTTCTGTCAAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA
M K T V F F I L L A T Y L A L H P G A A
CTGCAGTGCTATTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC
GACGTCACGATAAGTACGTGTCGTGTCTACTTGTTGTCTCTGACAGACTTACATGTCTTG
L Q C Y S C T A Q M N N R D C L N V Q N
TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA
ACGTCGGACCTGGTCGTGTCAACGAAATGTAGCGCGTAGGCCCGGTAACCTGAGCACTGT
C S L D Q H S C F T S R I R A I G L V T
GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTTGGGC
CAATAGTCATTCCCGACGTCGAGTGTCACACTCCTACTGAGCCTCTTGATGATAAACCCG
V I S K G C S S Q C E D D S E N Y Y L G
AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCCACACCCTG
TTCTTCTTGTAGTGCACGACGATGAGACTGGACACGTTACAGTTGCCCCGGGTGTGGGAC
K K N I T C C Y S D L C N V N G A H T L
AAGCCACCCACCACCCTGGGGCTGCTGACCGTGCTCTGCAGCCTGTTGCTGTGGGGCTCC
TTCGGTGGGTGGTGGGACCCCGACGACTGGCACGAGACGTCGGACAACGACACCCCGAGG
K P P T T L G L L T V L C S L L L W G S
AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC
TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCCTACTCGACGTG
S R L *
TCCACCCCACCCCCACACAGG
AGGTGGGGTGGGGGTGTGTCC

FIG. 3

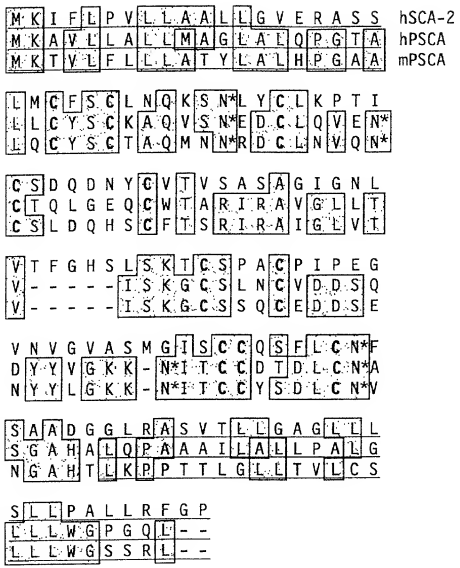
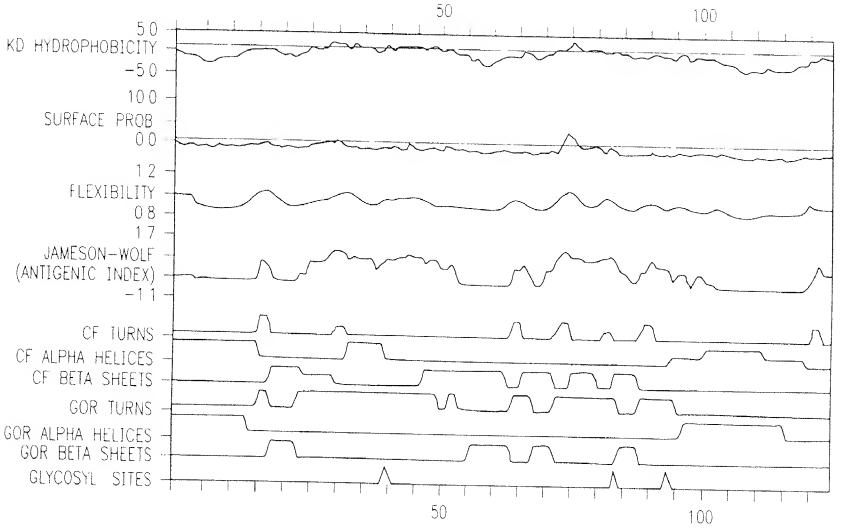


FIG. 4



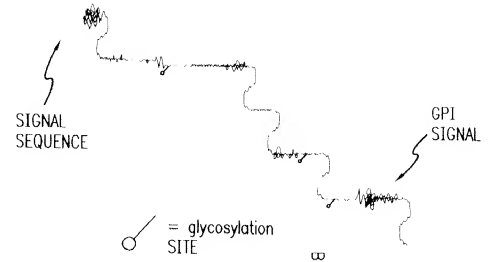


FIG. 5

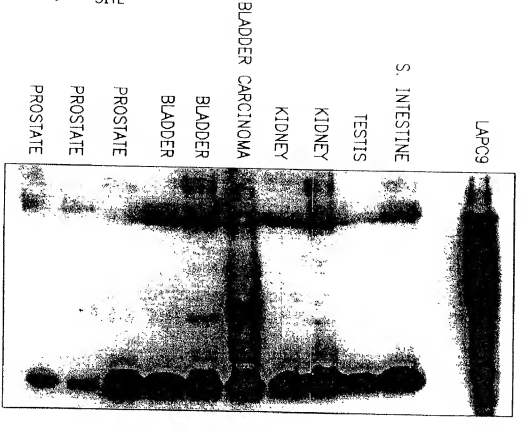
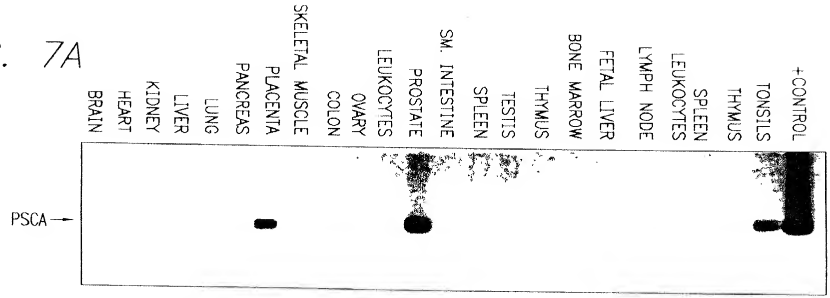


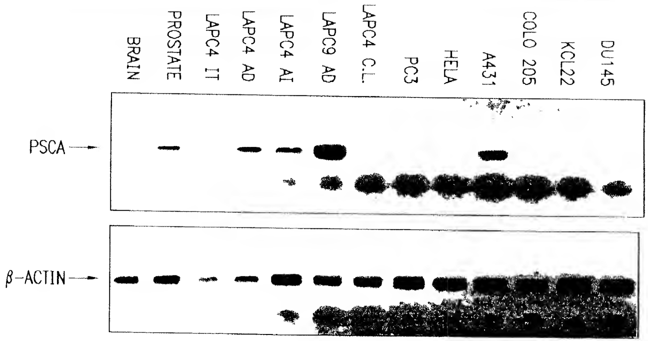
FIG. 6

FIG. 7A



BRAIN
HEART
KIDNEY
LIVER
LUNG
PANCREAS
PLACENTA
SKELETAL MUSCLE
COLON
OVARY
LEUKOCYTES
PROSTATE
SM. INTESTINE
SPLEEN
TESTIS
THYMUS
BONE MARROW
FETAL LIVER
LYMPH NODE
LEUKOCYTES
SPLEEN
THYMUS
TONSILS
+CONTROL
PSCA

FIG. 7B



BRAIN
PROSTATE
LAPC4 IT
LAPC4 AD
LAPC4 AI
LAPC9 AD
LAPC4 C.L.
PC3
HELA
A431
COLO 205
KCL22
DU145
PSCA
β-ACTIN

FIG. 8A

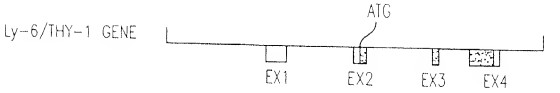


FIG. 8B

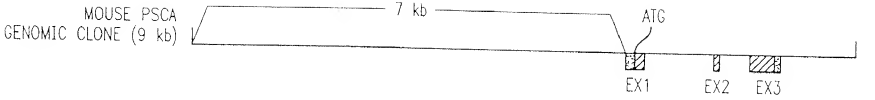


FIG. 8C

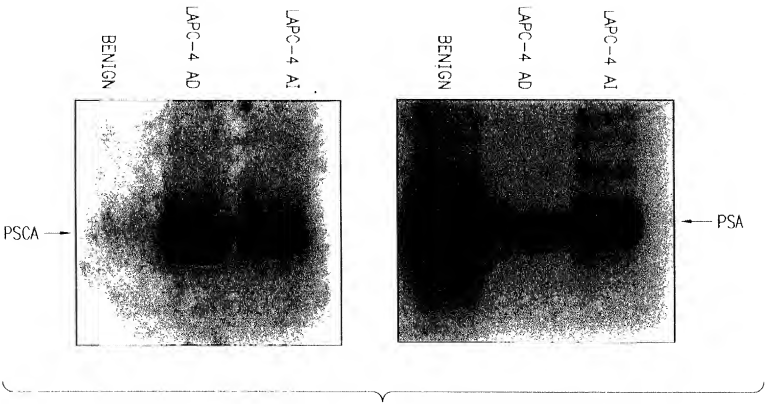


FIG. 9A

FIG. 9B

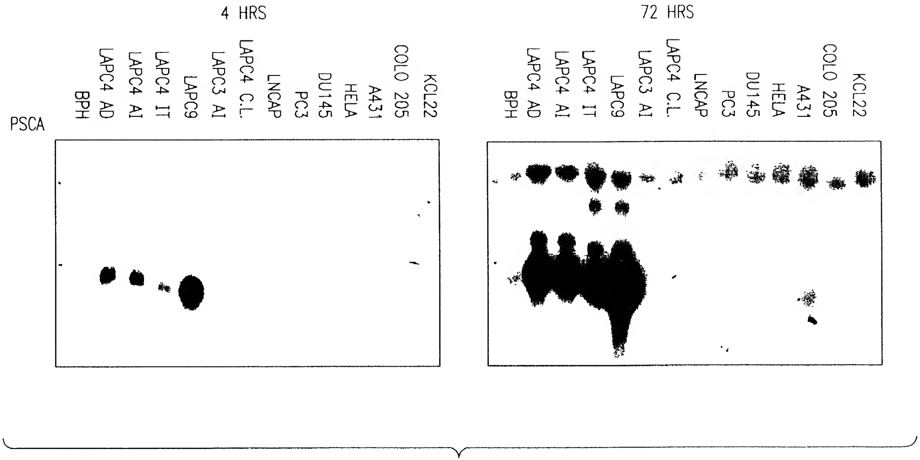

4 HRS
72 HRS
PSCA
BPH
LAPC4 AD
LAPC4 AI
LAPC4 IT
LAPC9
LAPC3 AI
LAPC4 C.L.
LNCAP
PC3
DU145
HELA
A431
COLO 205
KCL22

FIG. 10A

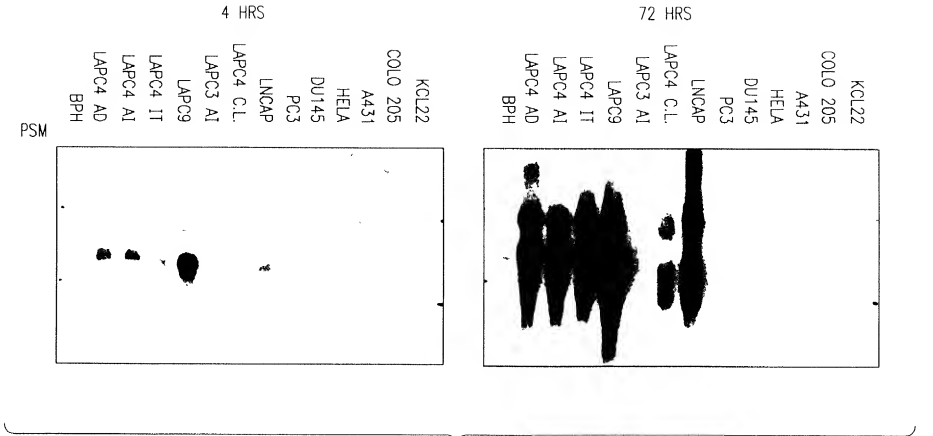


FIG. 10B

FIG. 10C

FIG. 11A

FIG. 11B

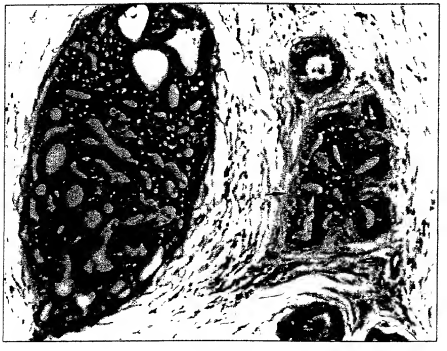
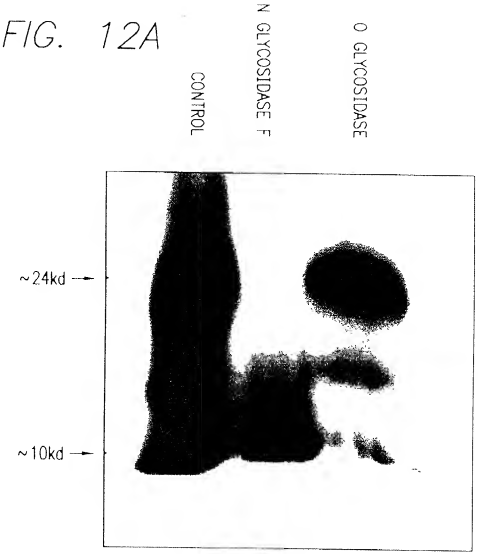


FIG. 11C

FIG. 12A



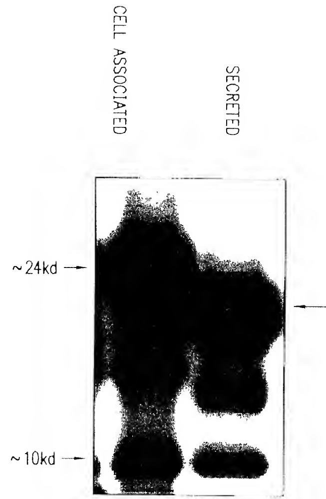


FIG. 12B

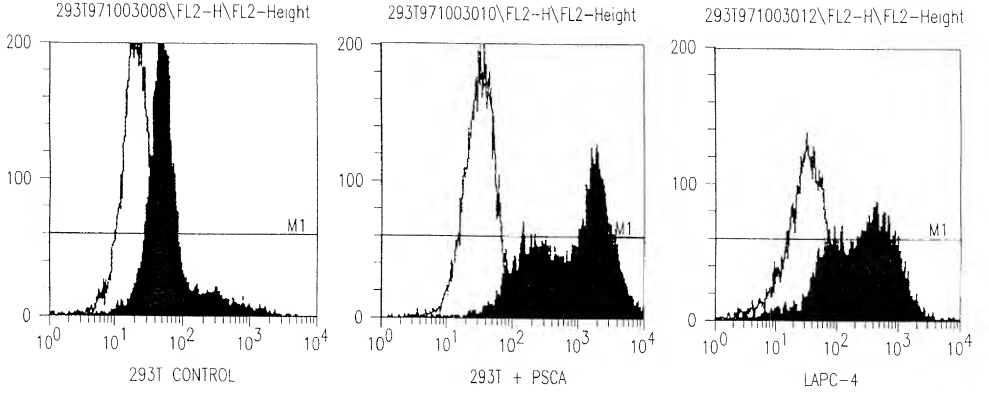


FIG. 12C

FIG. 13

FIG. 14A

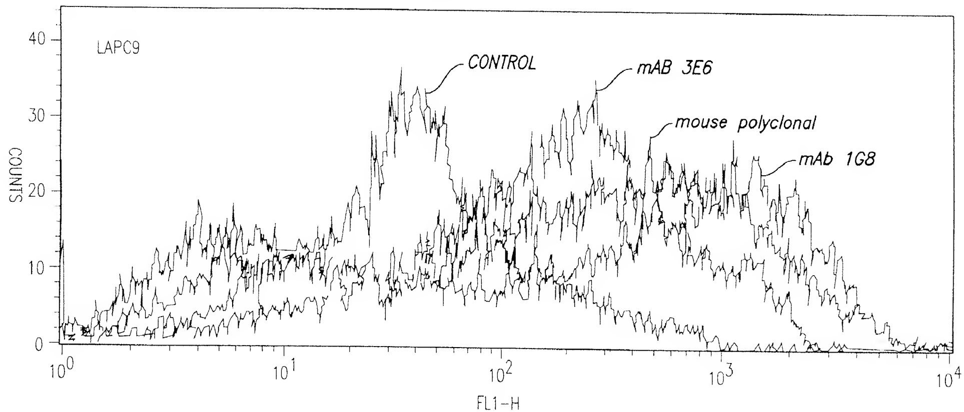


FIG. 14B

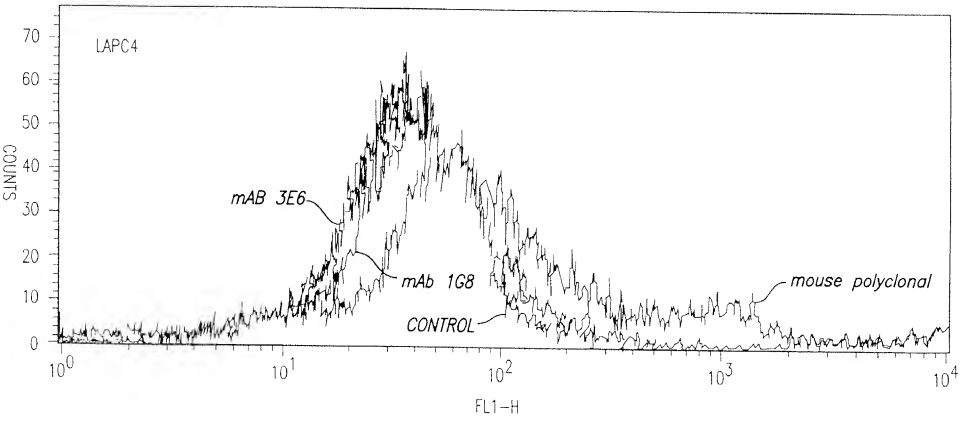
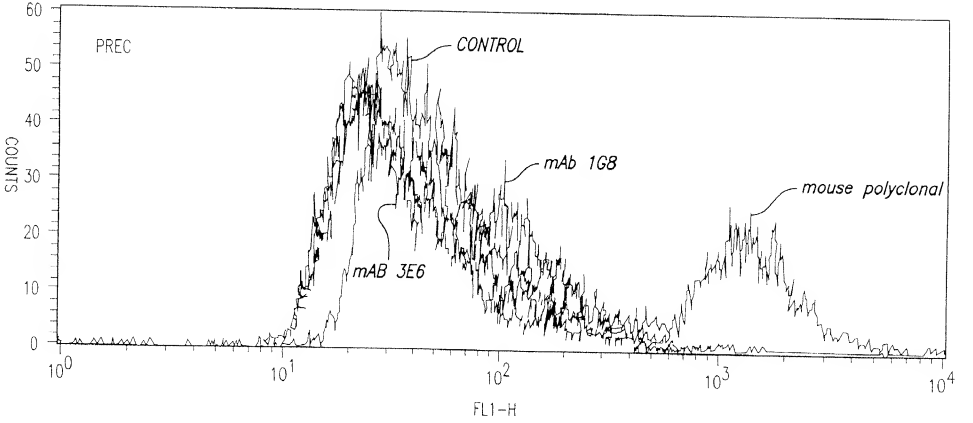

LAPC4
COUNTS
70
60
50
40
30
20
10
0
mAB 3E6
mAb 1G8
CONTROL
mouse polyclonal
10^0
10^1
10^2
10^3
10^4
FL1-H

FIG. 14C



EPITOPE MAP

mAb	ISOTYPE		FL (18–98)	N (2–50)	M (46–109)	C (85–123)
1G8	IgG1	k	2.039	0.007	0.628	0.000
2H9	IgG1	k	1.318	0.863	0.032	0.021
3C5	IgG2a	k	2.893	1.965	0.016	0.005
3E6	IgG3	k	0.328	0.024	0.069	0.370
4A10	IgG2a	k	2.039	1.315	0.000	0.014
2A2	IgG2a	k	1.366	0.733	0.010	0.003
3G3	IgG2a	k	2.805	1.731	0.004	0.000

FIG. 15A

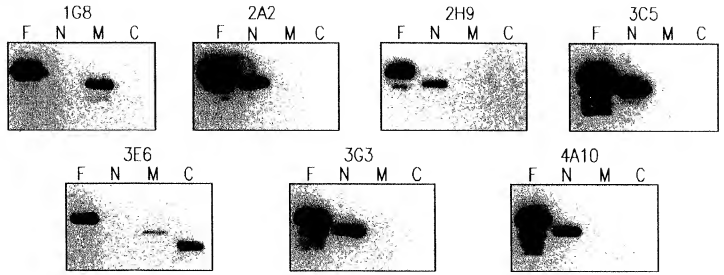


FIG. 15B

PROSTATE STEM CELL ANTIGEN (PSCA) IS A GPI-ANCHORED PROTEIN

```
1    M K I F L P V L L A A L L G V E R A S S    hSCA-2
1    M K A V L L A L L M A G L A L Q P G T A    hPSCA
1    M K T V L F L L L A T Y L A L H P G A A    mPSCA

21   L M C F S C L N Q K S N* L Y C L K P T I
21   L L C Y S C K A Q V S N* E D C L Q V E N*
21   L Q C Y S C T A Q M N N* R D C L N V Q N*

41   C S D Q D N Y C V T V S A S A G I G N L
41   C T Q L G E Q C W T A R I R A V G L L T
41   C S L D Q H S C F I S R I R A I G L V T

61   V T F G H S L S K T C S P A C P I P E G
61   V – – – – – – I S K G C S L N C V D D S Q
61   V – – – – – – I S K G C S S Q C E D D S E

81   V N V G V A S M G T S C C Q S F L C N* F
76   D Y Y V G K K – N* I T C C D T D L C N* A
76   N Y Y L G K K – N* I T C C Y S D L C N* V

101  S A A D G G L R A S V T L L G A G L L L
95   S G A H A L Q P A A A I L A L L P A L G
95   N G A H T L K P P T T L G L L T V L C S

121  S L L P A L L R F G P
115  L L L W G P G Q L – –
115  L L L W G S S R L – –
```

FIG. 16A

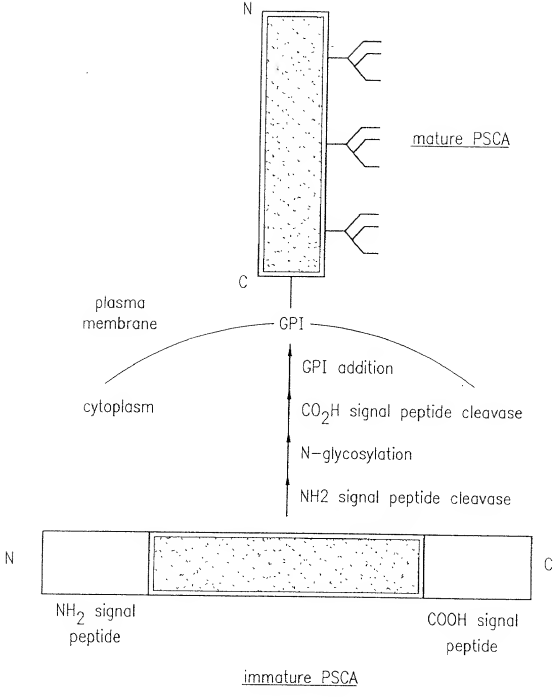

N
mature PSCA
C
plasma membrane
GPI
cytoplasm
GPI addition
CO_2H signal peptide cleavase
N–glycosylation
NH2 signal peptide cleavase
N
C
NH_2 signal peptide
COOH signal peptide
immature PSCA

FIG. 16B

FIG. 17

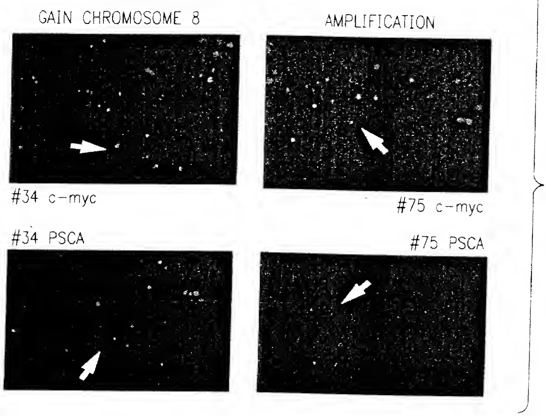

GAIN CHROMOSOME 8
AMPLIFICATION
#34 c-myc
#75 c-myc
#34 PSCA
#75 PSCA

FIG. 18

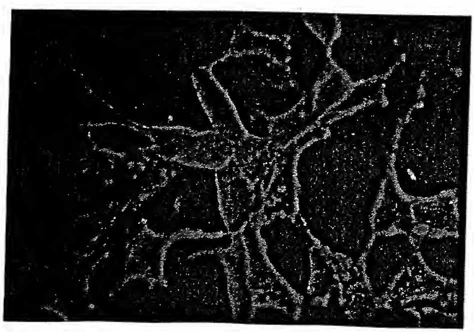


FIG. 19

FIG. 20

FIG. 21

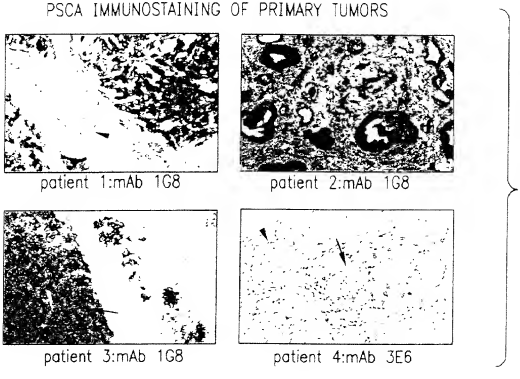

PSCA IMMUNOSTAINING OF PRIMARY TUMORS
patient 1:mAb 1G8
patient 2:mAb 1G8
patient 3:mAb 1G8
patient 4:mAb 3E6

FIG. 22

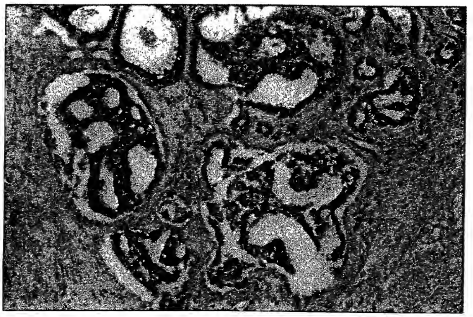


FIG. 23

FIG. 24

FIG. 25

FIG. 26

FIG. 27

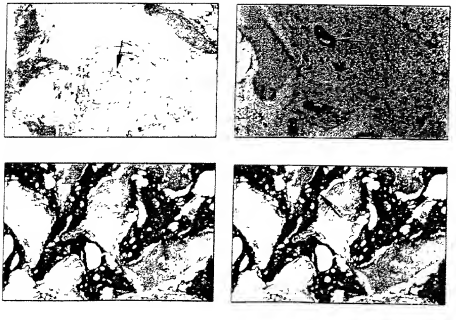


FIG. 28

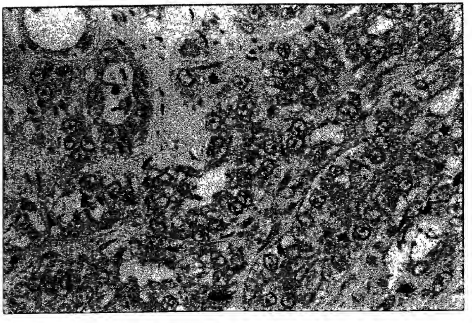
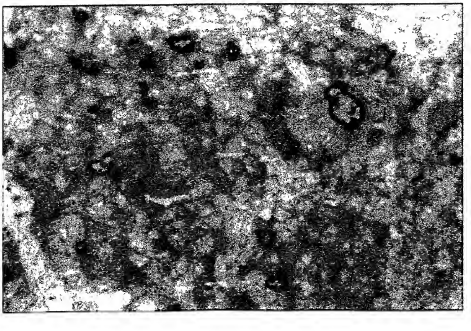


FIG. 29

FIG. 30



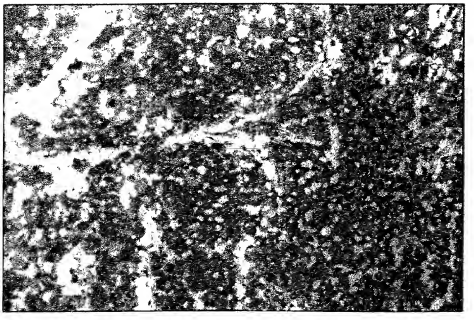


FIG. 31

FIG. 32

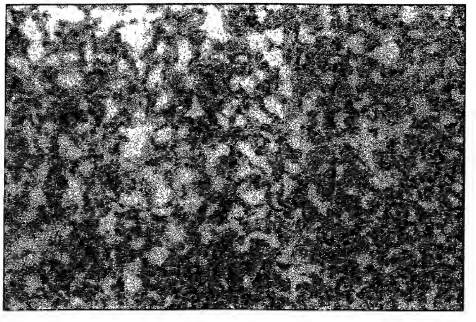
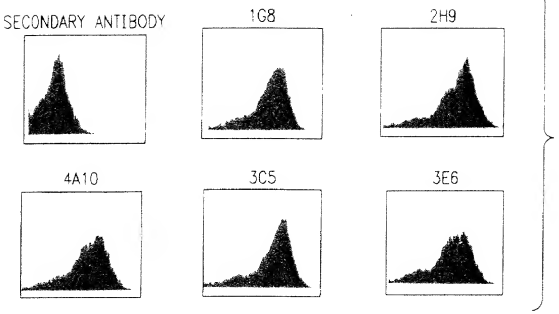


FIG. 33


SECONDARY ANTIBODY
1G8
2H9
4A10
3C5
3E6

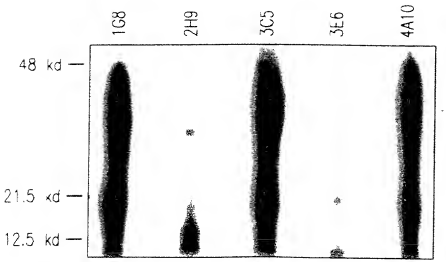

1G8
2H9
3C5
3E6
4A10
48 kd
21.5 kd
12.5 kd

FIG. 34

FIG. 35

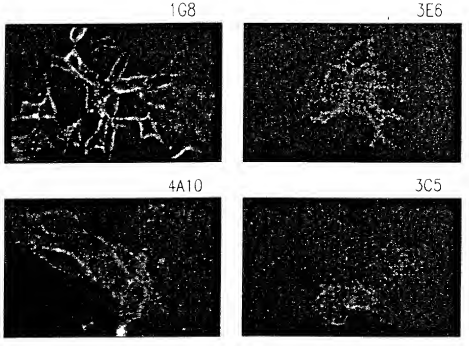


FIG. 36

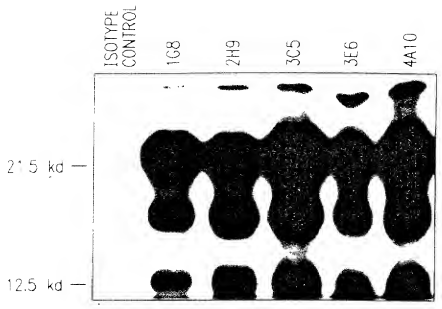


FIG. 37

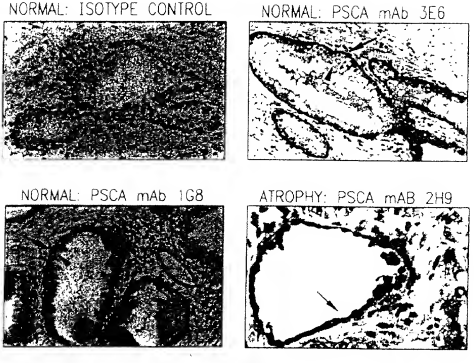
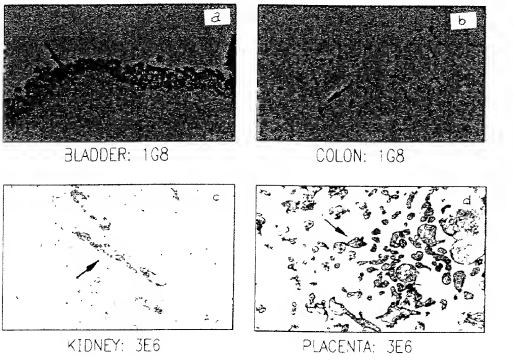


FIG. 38

FIG. 39A



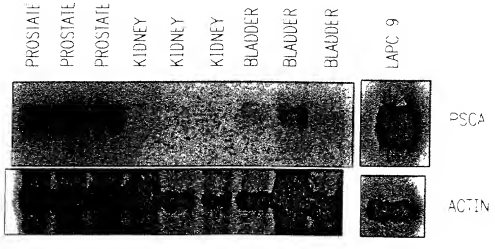
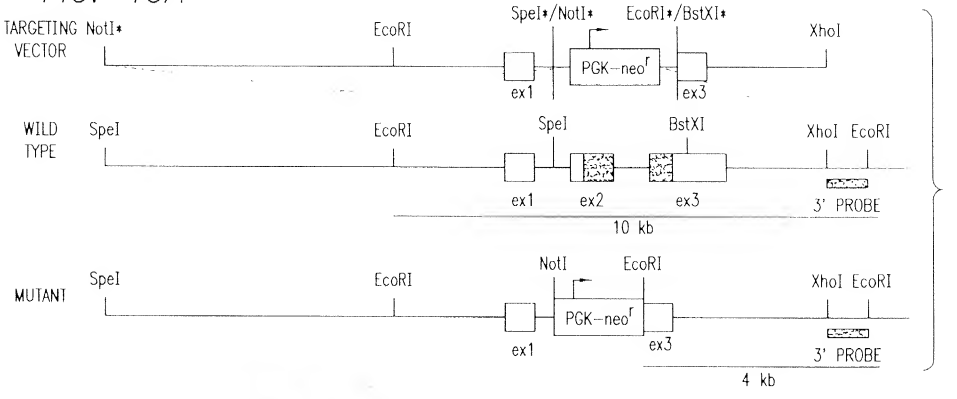


FIG. 39B

FIG. 40A



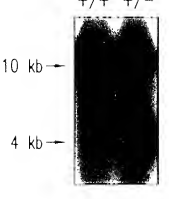


FIG. 40B

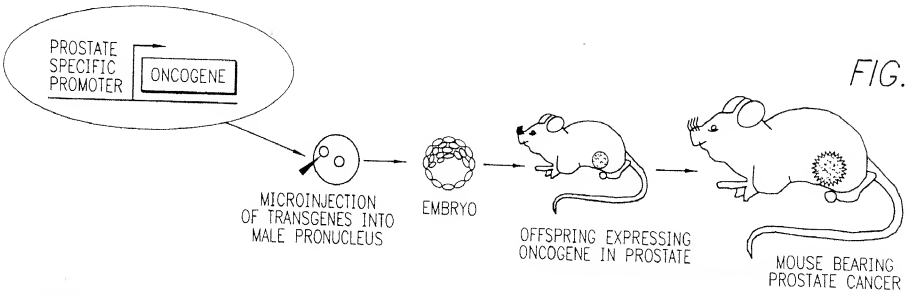


FIG. 41

TRANSGENE	TARGET TISSUES	CHARACTERISTICS
C3(1) (−3 kb)/ SV40 LARGE+SMALL, T MAROULAKOU et al. 1994 PNAS	PROSTATE (SECRETORY CELLS) URETHRAL, MAMMARY AND SWEAT GLAND	LOW−GRADE PIN 8−12 WKS HIGH−GRADE PIN 8−12 WKS INVASIVE CARCICINOMA 28 WKS NO METASTASES
PROBASIN (−426 bp)/ SV40 LARGE+SMALL, T GREENBERG et al. 1995 PNAS	PROSTATE (SECRETORY CELLS)	LOW−GRADE PIN 5−8 WKS HIGH−GRADE PIN 8−12 WKS INVASIVE CARCICINOMA 12 WKS METASTASES IN LYMPH NODE, LUNG, LIVER AND BONE
CRYPTIDIN2 (−6.5 kb)/ SV40 LARGE+SMALL, T GARABEDIAN et al. 1998 PNAS	PROSTATE (NEUROENDOCRINE CELLS) SMALL INTESTINE	LOW−GRADE PIN 8−12 WKS HIGH−GRADE PIN 8−12 WKS INVASIVE CARCICINOMA 16 WKS METASTASES IN LYMPH NODE, LUNG, LIVER, AND BONE

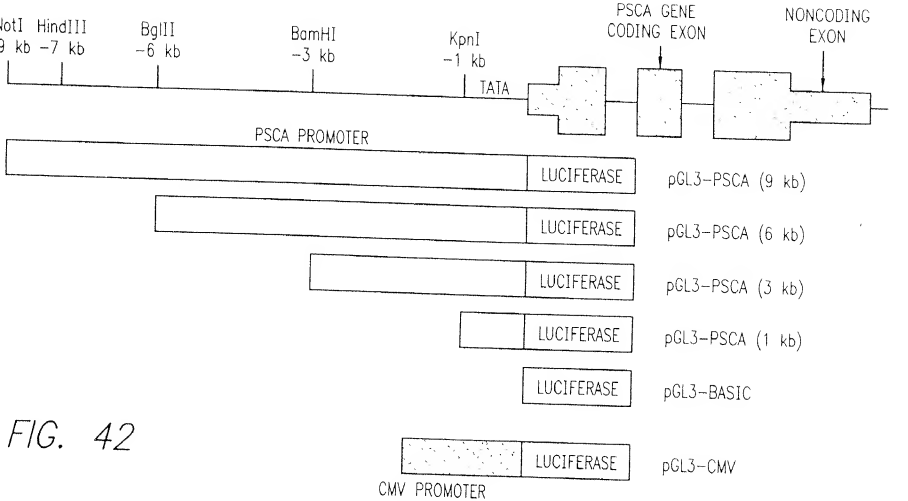


FIG. 42

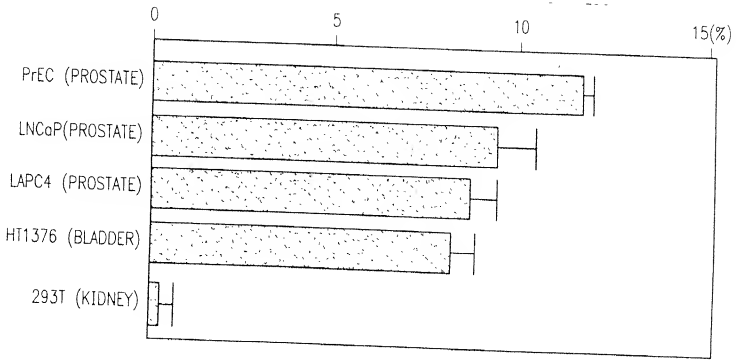


FIG. 43

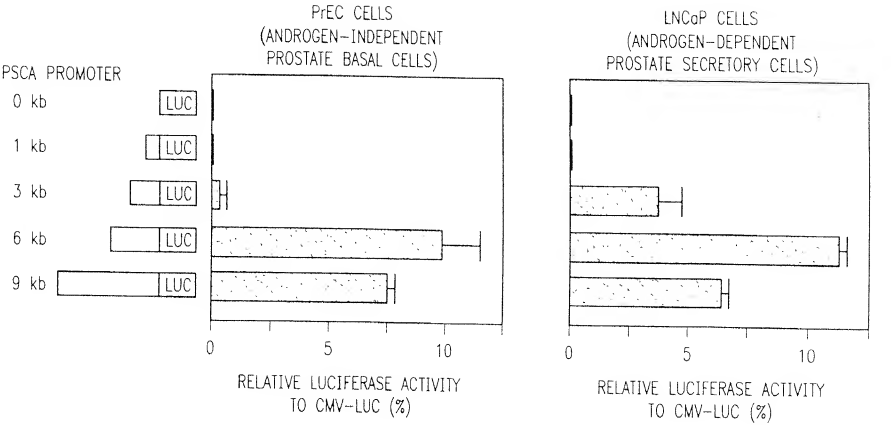
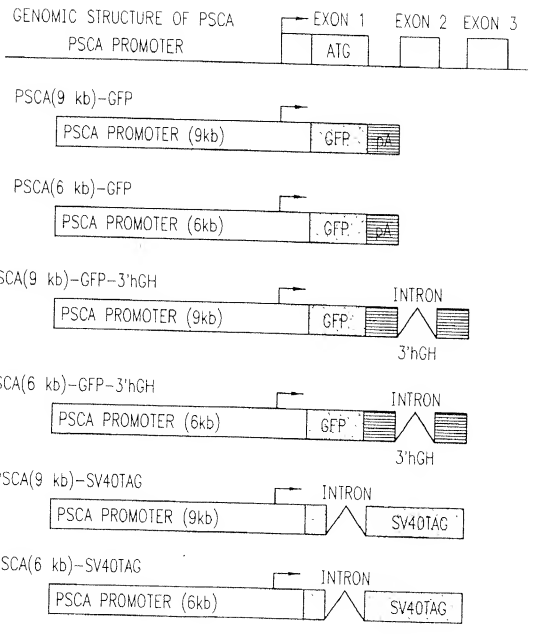

PrEC CELLS
(ANDROGEN-INDEPENDENT
PROSTATE BASAL CELLS)
PSCA PROMOTER
0 kb
1 kb
3 kb
6 kb
9 kb
LUC
0
5
10
RELATIVE LUCIFERASE ACTIVITY
TO CMV-LUC (%)
LNCaP CELLS
(ANDROGEN-DEPENDENT
PROSTATE SECRETORY CELLS)
0
5
10
RELATIVE LUCIFERASE ACTIVITY
TO CMV-LUC (%)

FIG. 44

FIG. 45



NUMBER OF FOUNDERS (DNA POSITIVE)
2
1
6
8
3
9

NEGATIVE TISSUES
STOMACH
SMALL INTESTINE
COLON
SEMINAL VESICLE
URETHRA
TESTIS
LIVER
KIDNEY
LUNG
BRAIN
HEART
SKELETAL MUSCLE
OVARY
UTERUS

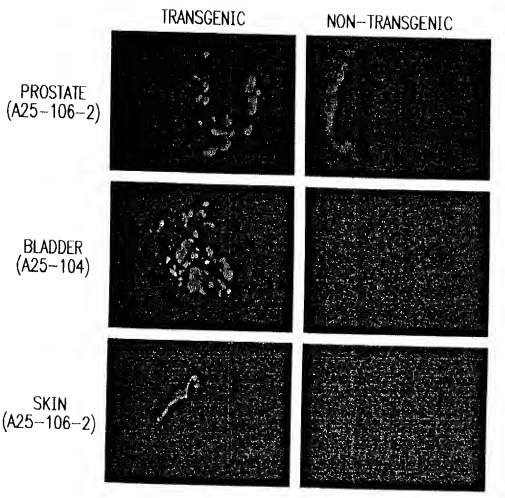
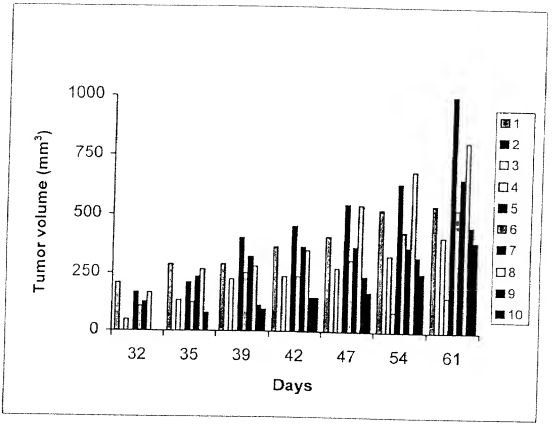


FIG. 46

FIG. 47

FIG. 48


1000
750
500
250
0
Tumor volume (mm3)
32
35
39
42
47
54
61
Days
1
2
3
4
5
6
7
8
9
10

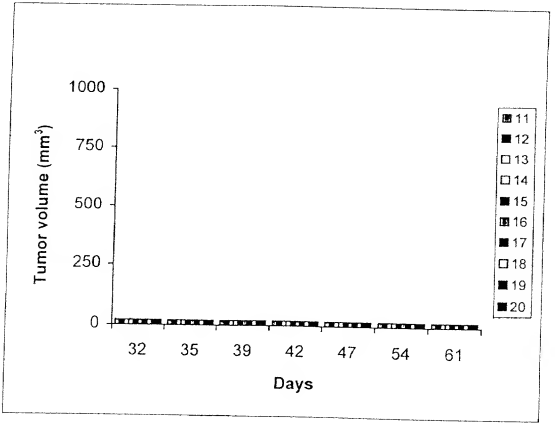

1000
750
500
250
0
Tumor volume (mm3)
32
35
39
42
47
54
61
Days
11
12
13
14
15
16
17
18
19
20

FIG. 49

A

mAb	Isotype		Epitope recognized (OD 450 nm) F (18-98)	N (2-50)	M (46-109)	C (85-123)
1G8	IgG1	k	**1.485**	0.004	**1.273**	0.003
2A2	IgG2a	k	**0.973**	**0.631**	0.023	0.010
2H9	IgG1	k	**1.069**	**1.026**	0.002	0.001
3C5	IgG2a	k	**1.916**	**1.709**	0.006	0.002
3E6	IgG3	k	**1.609**	0.036	**1.133**	**2.118**
3G3	IgG2a	k	**2.805**	**1.731**	0.004	0.000
4A10	IgG2a	k	**1.053**	**0.493**	0.000	0.001

B

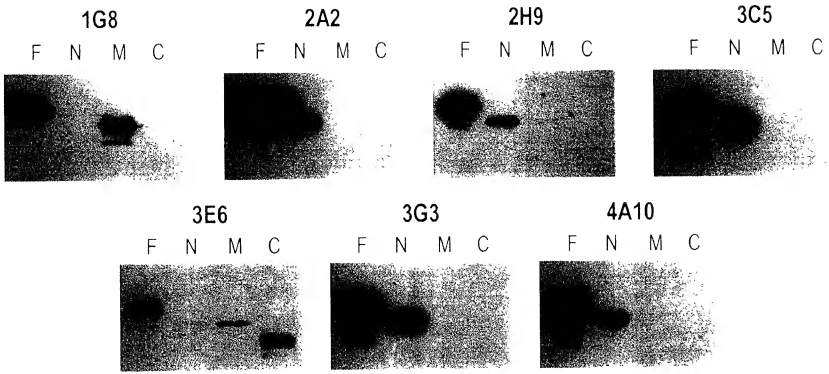


FIG. 50

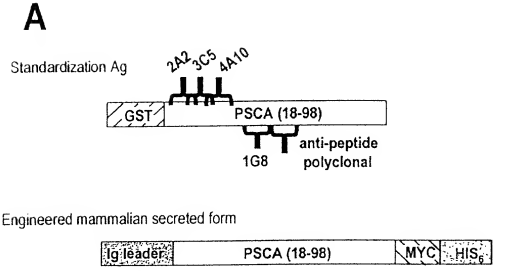
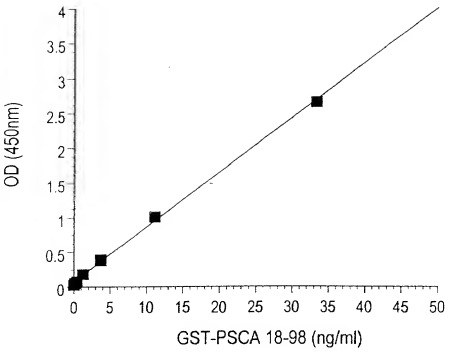

A
Standardization Ag
2A2
3C5
4A10
GST
PSCA (18-98)
1G8
anti-peptide
polyclonal
Engineered mammalian secreted form
Ig leader
PSCA (18-98)
MYC
HIS6
B
Anti-IgG2a HRP
Anti-PSCA mAbs 3C5+4A10+2A2 (IgG2a)
PSCA
Affinity purified anti-peptide polyclonal
+ mAb 1G8 (IgG1)

FIG. 51

A



B

Sample	OD+range (n=2)	ng/ml
vector	0.005+0.001	ND
vector+hu serum	0.004+0.001	ND
secPSCA	2.695+0.031	32.92
secPSCA+hu serum	2.187+0.029	26.55

FIG. 52

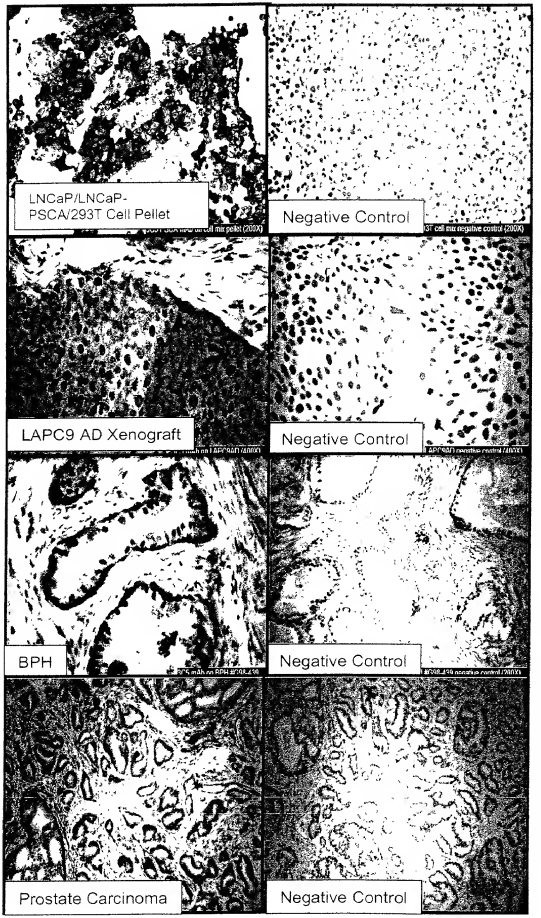


FIG. 53

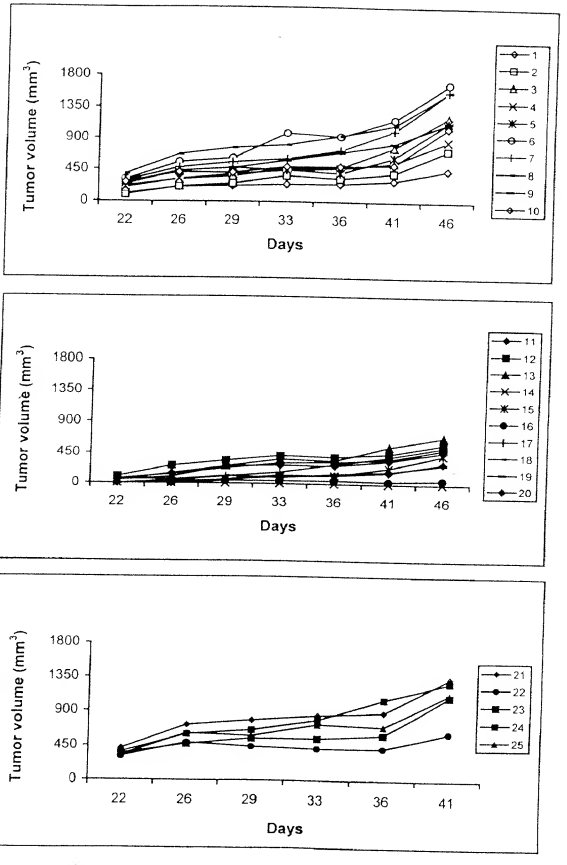
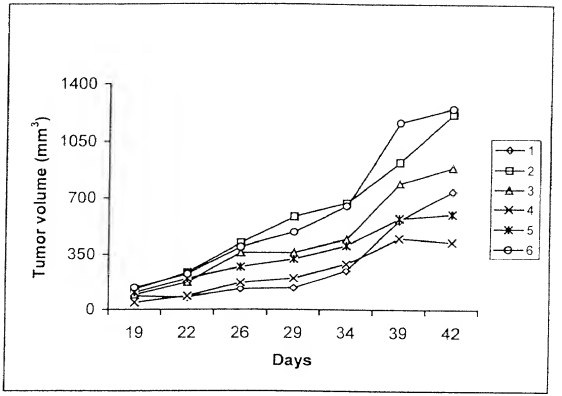

Tumor volume (mm3)
1800
1350
900
450
0
22
26
29
33
36
41
46
Days
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25

FIG. 54


1400
1050
700
350
0
Tumor volume (mm3)
19
22
26
29
34
39
42
Days
1
2
3
4
5
6

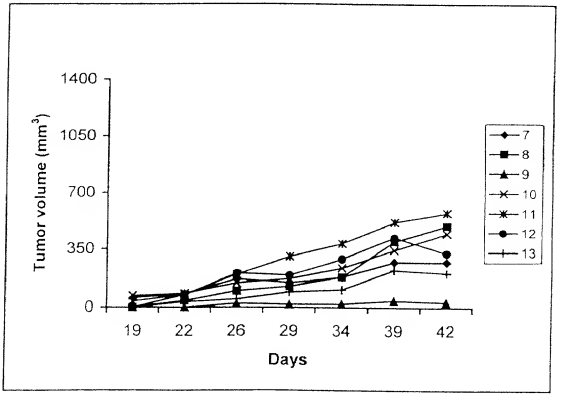
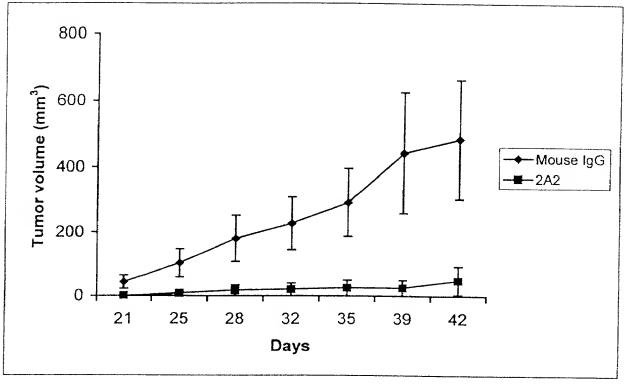

1400
1050
700
350
0
Tumor volume (mm3)
19
22
26
29
34
39
42
Days
7
8
9
10
11
12
13

FIG. 55


800
600
400
200
0
Tumor volume (mm3)
21
25
28
32
35
39
42
Days
Mouse IgG
2A2

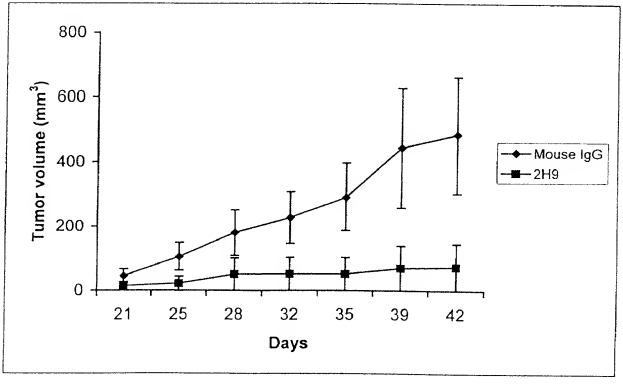
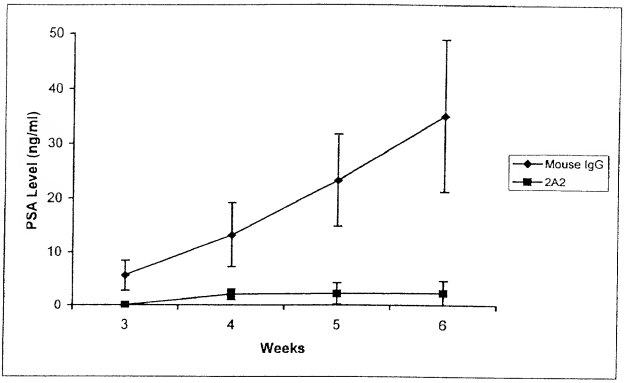

800
600
400
200
0
Tumor volume (mm3)
21
25
28
32
35
39
42
Days
Mouse IgG
2H9

FIG. 56


50
40
30
20
10
0
PSA Level (ng/ml)
3
4
5
6
Weeks
Mouse IgG
2A2

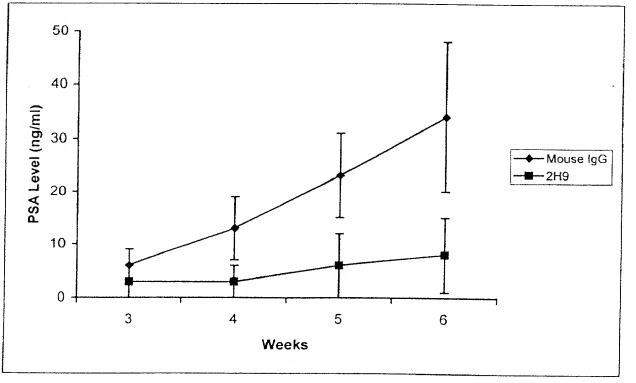

50
40
30
20
10
0
PSA Level (ng/ml)
3
4
5
6
Weeks
Mouse IgG
2H9

FIG. 57

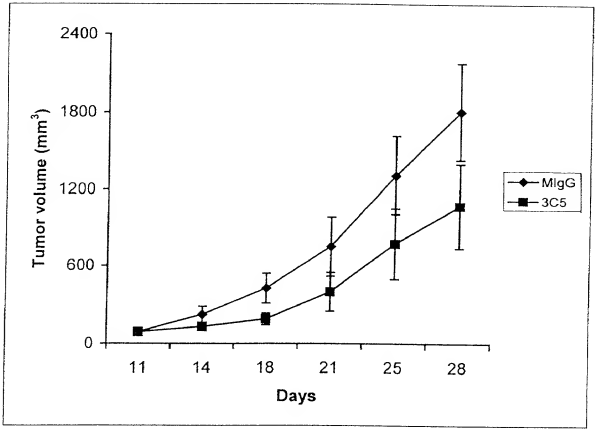

2400
1800
1200
600
0
Tumor volume (mm3)
11
14
18
21
25
28
Days
MIgG
3C5

FIG. 58

```
TGCTTCTTCCTGATGGCAGTGGTTATAGGAGTCAATTCAGAGGTTCAGCTGCAGCAGTCT  60
 C  F  F  L  M  A  V  V  I  G  V  N  S  E  V  Q  L  Q  Q  S   20

                                                      ┌──────
GGGGCAGAACTTGTGAGGTCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGGCTTC 120
 G  A  E  L  V  R  S  G  A  S  V  K  L  S  C  T  A  S  G  F   40

 ──────── CDR1 ──────┐
AACATTAAAGACTACTATATACACTGGGTGAATCAGAGGCCTGACCAGGGCCTGGAGTGG 180
 N  I  K  D  Y  Y  I  H  W  V  N  Q  R  P  D  Q  G  L  E  W   60

          ┌──────────────────────── CDR2 ──────────────────────┐
ATTGGATGGATTGATCCTGAGAATGGTGACACTGAATTTGTCCCGAAGTTCCAGGGCAAG 240
 I  G  W  I  D  P  E  N  G  D  T  E  F  V  P  K  F  Q  G  K   80

GCCACTATGACTGCAGACATTTTCTCCAACACAGCCTACCTGCACCTCAGCAGCCTGACA 300
 A  T  M  T  A  D  I  F  S  N  T  A  Y  L  H  L  S  S  L  T  100

                                    ┌ CDR3 ┐
TCTGAAGACACTGCCGTCTATTACTGTAAAACGGGGGGTTTCTGGGGCCAAGGGACTCTG 360
 S  E  D  T  A  V  Y  Y  C  K  T  G  G  F  W  G  Q  G  T  L  120

GTCACTGTCTCTGCAGCCAAAACGACACCCCCATCTGTCTATCCACTG
 V  T  V  S  A  A  K  T  T  P  P  S  V  Y  P  L
```

FIG. 59

```
TTGGTAGCAACAGCCTCAGATGTCCACTCCCAGGTCCAACTGCAGCAACCTGGGTCTGAA  60
 L  V  A  T  A  S  D  V  H  S  Q  V  Q  L  Q  Q  P  G  S  E   20

CTGGTGAGGCCTGGAACTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTATACATTCTCC 120
 L  V  R  P  G  T  S  V  K  L  S  C  K  A  S  G  Y  T  F  S   40
                                              CDR1

AGCTACTGGATGCACTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGATTGGAAAT 180
 S  Y  W  M  H  W  V  K  Q  R  P  G  Q  G  L  E  W  I  G  N   60

ATTGACCCTGGTAGTGGTTACACTAACTACGCTGAGAACCTCAAGACCAAGGCCACACTG 240
 I  D  P  G  S  G  Y  T  N  Y  A  E  N  L  K  T  K  A  T  L   80
          CDR2

ACTGTAGACACATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC 300
 T  V  D  T  S  S  S  T  A  Y  M  Q  L  S  S  L  T  S  E  D  100

TCTGCAGTCTATTACTGTACAAGCCGATCTACTATGATTACGACGGGATTTGCTTACTGG 360
 S  A  V  Y  Y  C  T  S  R  S  T  M  I  T  T  G  F  A  Y  W  120
                                 CDR3

GGCCAAGGGACTCTGGTCACTGTCTCTGCAGCTACAACAACAGCCCCATCTGTCTATCCA 420
 G  Q  G  T  L  V  T  V  S  A  A  T  T  T  A  P  S  V  Y  P  160

CTGGCC
 L  A
```

FIG. 60

```
AATGACTTCGGGTTGAGCTGGGTTTTTATTATTGTTCTTTTAAAAGGGGTCCGGAGTGAA   60
 N  D  F  G  L  S  W  V  F  I  I  V  L  L  K  G  V  R  S  E    20

GTGAGGCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCC  120
 V  R  L  E  E  S  G  G  G  W  V  Q  P  G  G  S  M  K  L  S    40

TGTGTAGCCTCTGGATTTACTTTCAGTAATTACTGGATGACTTGGGTCCGCCAGTCTCCA  180
 C  V  A  S  G  F  T  F  S  N  Y  W  M  T  W  V  R  Q  S  P    60
             ______________________________
                          CDR1

GAGAAGGGGCTTGAGTGGGTTGCTGAAATTCGATTGAGATCTGAAAATTATGCAACACAT  240
 E  K  G  L  E  W  V  A  E  I  R  L  R  S  E  N  Y  A  T  H    80
                         ___________________________________
                                             CDR2

TATGCGGAGTCTGTGAAAGGGAAATTCACCATCTCAAGAGATGATTCCAGAAGTCGTCTC  300
 Y  A  E  S  V  K  G  K  F  T  I  S  R  D  D  S  R  S  R  L   100
_____________________

TACCTGCAAATGAACAACTTAAGACCTGAAGACAGTGGAATTTATTACTGTACAGATGGT  360
 Y  L  Q  M  N  N  L  R  P  E  D  S  G  I  Y  Y  C  T  D  G   120
                                                          __

CTGGGACGACCTAACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACA  420
 L  G  R  P  N  W  G  Q  G  T  L  V  T  V  S  A  A  K  T  T   140
_______________
     CDR3

CCCCCATCTGTCTATCCACTGGCCCCTTGTGTA
 P  P  S  V  Y  P  L  A  P  C  V
```

FIG. 61

CDR1 Comparisons

1G8	lgG$_{1k}$	Middle	G	F	N	I	K	D	Y	Y	I	H
2H9	lgG$_{1k}$	N-Term.	G	F	T	F	S	N	Y	W	M	T
4A10	lgG$_{2ak}$	N-Term.	G	Y	T	F	S	S	Y	W	M	H

CDR2 Comparisons

1G8	lgG$_{1k}$	W	I	D	P	E	N	G	D	T	E	F	V	P	K	F	Q	G		
2H9	lgG$_{1k}$	E	I	R	L	R	S	E	N	Y	A	T	H	Y	A	E	S	V	K	G
4A10	lgG$_{2ak}$	N	I	D	P	G	S	G	Y	T	N			Y	A	E	N	L	K	T

CDR3 Comparisons

1G8	lgG$_{1k}$	G	G	F								
2H9	lgG$_{1k}$	L	G	R	P	N						
4A10	lgG$_{2ak}$	R	S	T	M	I	T	T	G	F	A	Y

FIG. 62

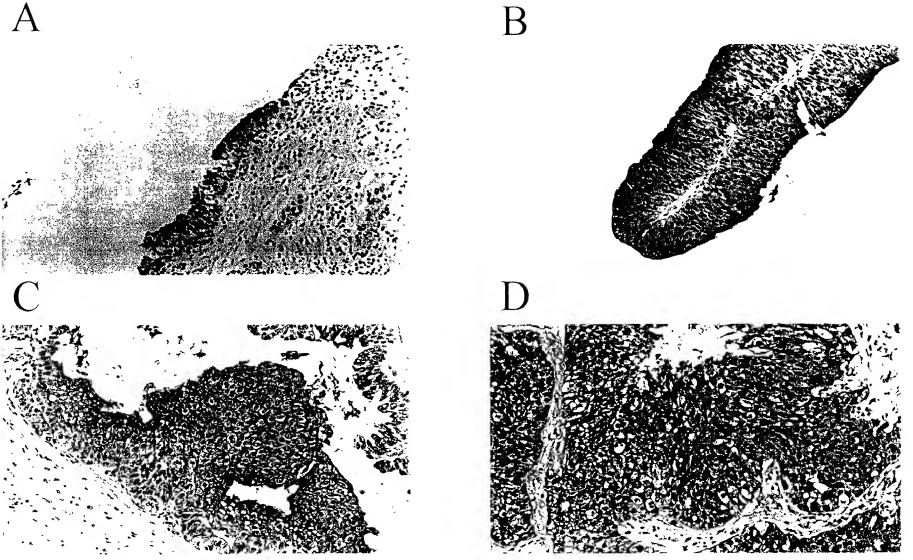


FIG. 63

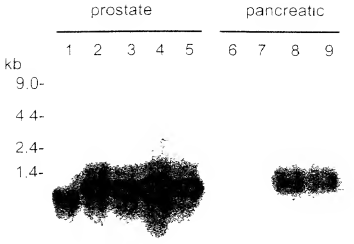


FIG. 64

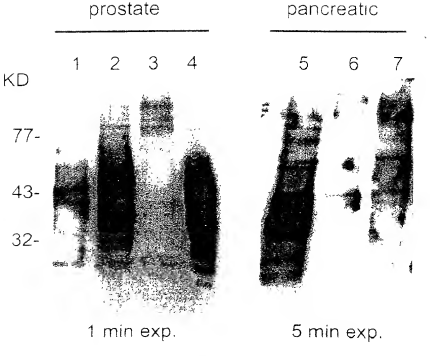
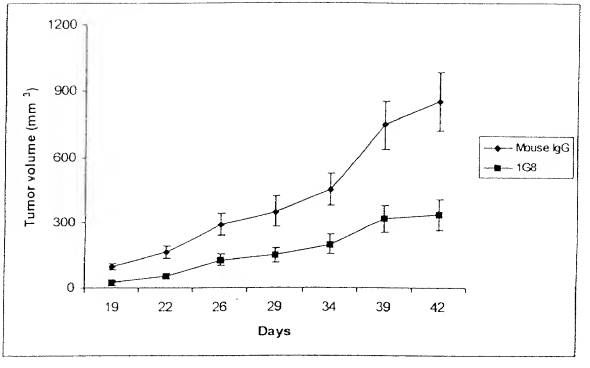


FIG. 65


1200
900
600
300
0
Tumor volume (mm 3)
19
22
26
29
34
39
42
Days
Mouse IgG
1G8

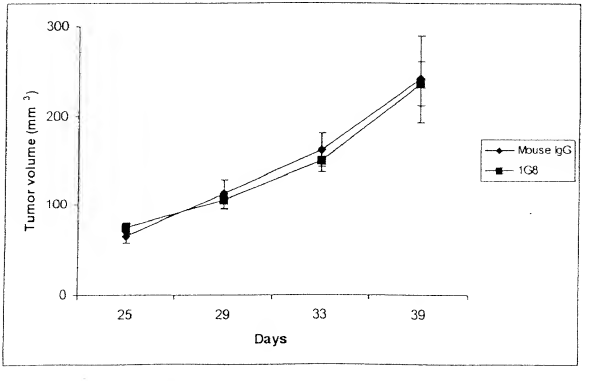
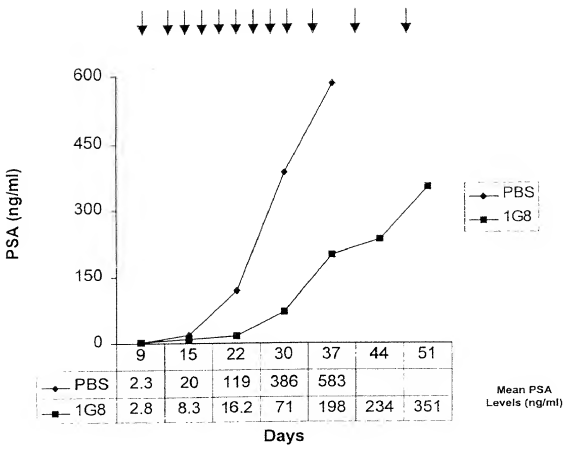

300
200
100
0
Tumor volume (mm 3)
25
29
33
39
Days
Mouse IgG
1G8

FIG. 66

A)


600
450
300
150
0
PSA (ng/ml)
PBS
1G8
9 15 22 30 37 44 51
PBS 2.3 20 119 386 583
1G8 2.8 8.3 16.2 71 198 234 351
Mean PSA Levels (ng/ml)
Days

B)

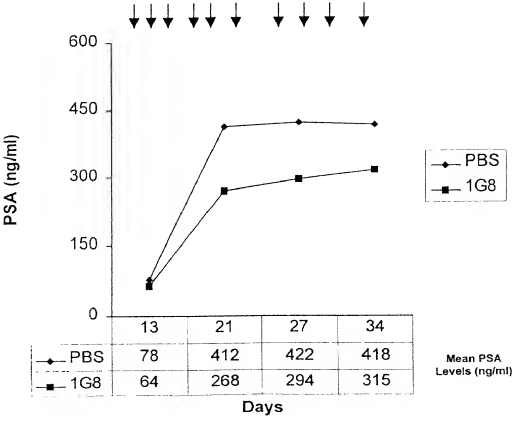
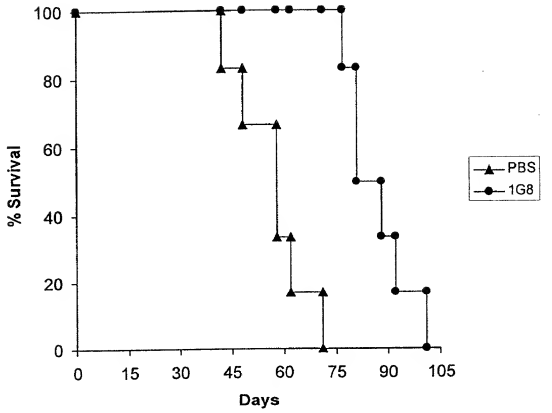

600
450
300
150
0
PSA (ng/ml)
PBS
1G8
13 21 27 34
PBS 78 412 422 418
1G8 64 268 294 315
Mean PSA Levels (ng/ml)
Days

FIG. 67

A)


100
80
60
40
20
0
% Survival
0
15
30
45
60
75
90
105
Days
PBS
1G8

B)

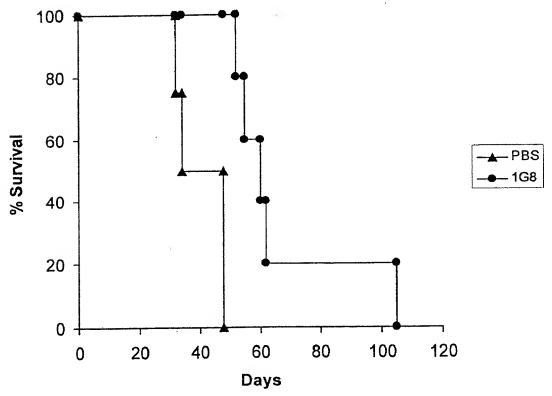
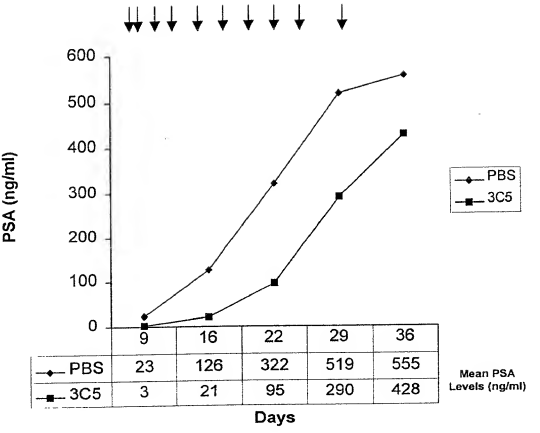

100
80
60
40
20
0
% Survival
0
20
40
60
80
100
120
Days
PBS
1G8

FIG. 68

A)

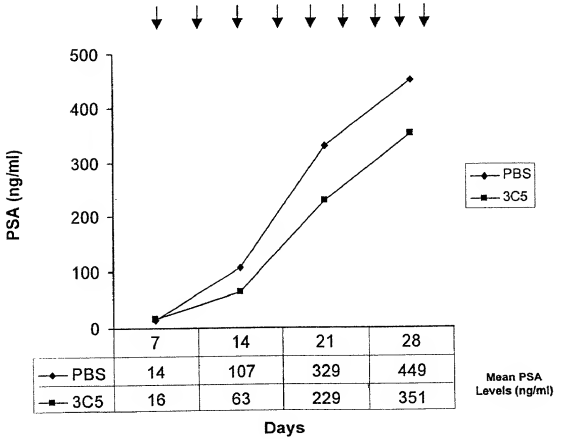


	9	16	22	29	36
PBS	23	126	322	519	555
3C5	3	21	95	290	428

Mean PSA Levels (ng/ml)

Days

B)



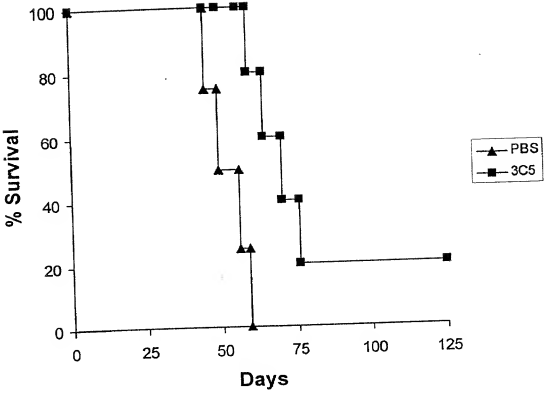
	7	14	21	28
PBS	14	107	329	449
3C5	16	63	229	351

Mean PSA Levels (ng/ml)

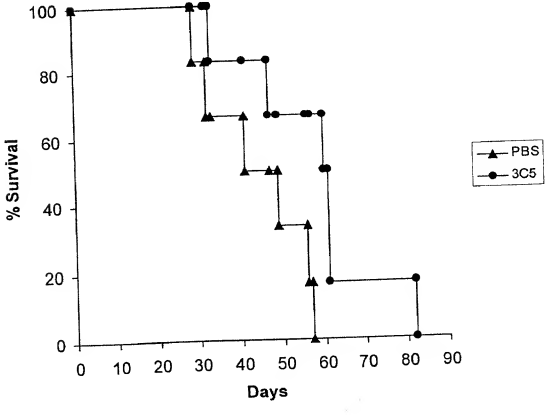
Days

FIG. 69

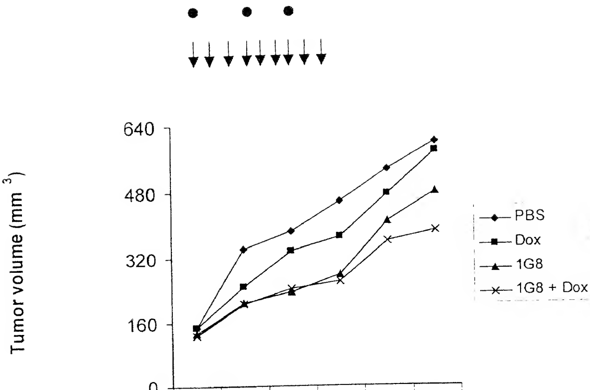
A)


100
80
60
40
20
0
% Survival
0
25
50
75
100
125
Days
PBS
3C5

B)


100
80
60
40
20
0
% Survival
0
10
20
30
40
50
60
70
80
90
Days
PBS
3C5

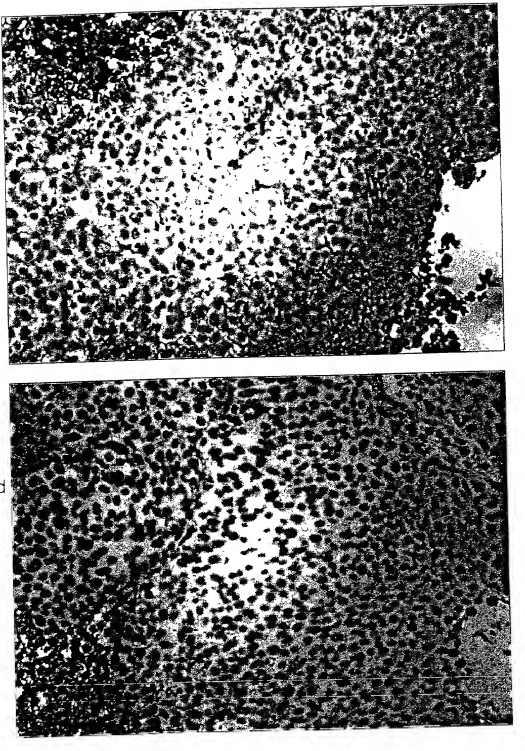
F I G. 70



	9	15	23	29	36	43
PBS	149	343	385	458	533	601
Dox	148	250	337	371	473	577
1G8	135	208	235	276	408	479
1G8 + Dox	129	205	242	260	359	387

Days

FIG. 71



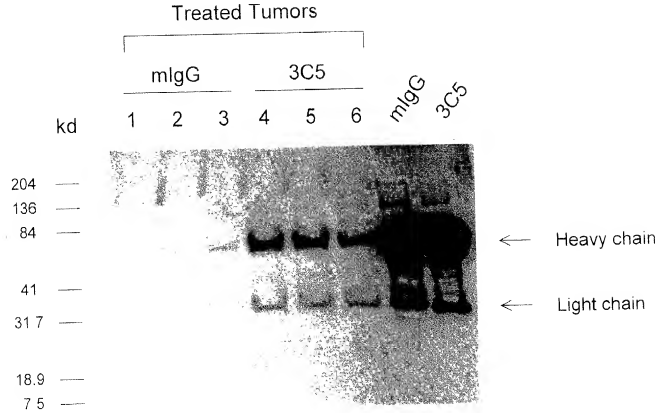

Treated Tumors
mIgG
3C5
kd
1
2
3
4
5
6
mIgG
3C5
204
136
84
41
31 7
18.9
7 5
Heavy chain
Light chain

FIG. 72

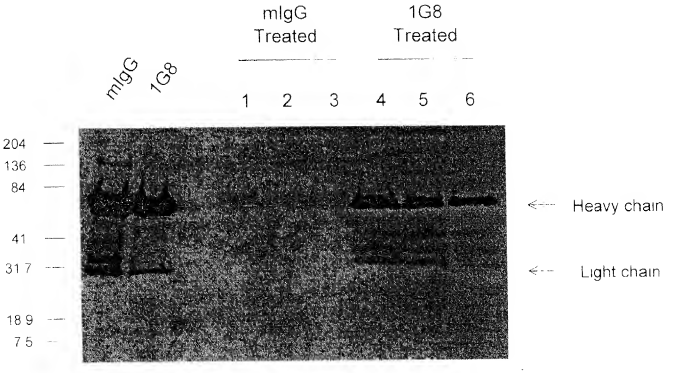


FIG. 73